

1		50
AtBI-1	(1)	-----MDAFSSFFDSQPGS---RSWSYDSLKNFRQISPAVQNHLLK
BnBI-1	(1)	-----MDSFSSFFDSQPGS---RSWSYDSLKNLRQISPSVQNHLLK
GmBI2	(1)	-----RLQAMDAFNSFFDS-----RNRWNYDTLKNFRQISPVVQNHLLKQ
GmBI3	(1)	ITKTIRFDSLFSMDTFFKSPSSSSSRWSYDTLKNFREISPLVQNHLLK
HVBI-1	(1)	-----MDAFYSTS---SAAASGWGHDSLKNFRQISPAVQSHLLK
NtBI-1	(1)	-----MESCTSFNSQSASS-RNRWSYDSLKNFRQISPFVQTHLLK
OsBI-1	(1)	-----MDAFYSTSSAYGAAASGWGYDSLKNFRQISPAVQSHLLK
TaBI11	(1)	-----
TaBI18	(1)	-----FSGTFRNSRSDDFVLCELQRELPRCRDATLTV
TaBI5 new	(1)	-----VAMPGR
ZmBI14	(1)	-----
ZmBI16	(1)	-----
ZmBI33	(1)	-----
ZmBI8	(1)	-----
Consensus	(1)	F S W YDSLKN R ISP VQ HLK
	51	100
AtBI-1	(39)	VYLTLCALVASAFGAYLHVLWNIGGILTTIGCIGTMIWLLSCPPYEHQK
BnBI-1	(39)	VYLTLCALVASAFGAYLHVLWNIGGILTTIGCFGSMIWLLSCPPYEQK
GmBI2	(40)	VYFTLCFAVVAAVGAFLHVLWNIGGFLTTVACMGSSFLLSTPPFEERK
GmBI3	(51)	VYFTLCFAVVAAVGAFLHVLWNIGGFLTTLASIGSMFWLLSTPPFEERK
HVBI-1	(37)	VYLTLCFALASSAVGAYLHIALNIGGMLTMLACVGTIAWMFVSPVYEERK
NtBI-1	(41)	VYLSLCCALVASAAGAYLHILWNIGGLTTLGCVGSIVWLMATPLYEEQK
OsBI-1	(40)	VYLTLCVALAASAVGAYLHVALNIGGMLTMLGCVGSIAWLFSVPVFEERK
TaBI11	(1)	-----
TaBI18	(33)	VYVIPIVGRIKSAAGAYLHIALNIGGMLTMLACIGTIAWMFVSPVYEERK
TaBI5 new	(7)	RFRLTYALPGLICRGCLPAHCPEHWRDADNARVYRNHRLDVLGASLRGEE
ZmBI14	(1)	-----GSIWLFSVPVYEERK
ZmBI16	(1)	-----WNIGVRLTMLGCIGSIDWLFSVPVYEERK
ZmBI33	(1)	-----WNIGGTLTMLGCVGSIAWLFSVPVYEERK
ZmBI8	(1)	-----
Consensus	(51)	VY TLC AL ASA GAYLHV NIGG LT LGCIGSI WL S PVYEERK
	101	150
AtBI-1	(89)	RLSLLFVSAVLEGASVGPLIKVAIDVDPSILITAFVGTIAIAFVCFSAAM
BnBI-1	(89)	RLSLLFLSAVLEGASVGPLIKVAVDVDFPSILITAFVGTIAIAFICFSGAAM
GmBI2	(90)	RVTLLMAASLFQGSIGPLIDLAIHIDPSLIFSAFVGTALAFACFSGAAL
GmBI3	(101)	RLSLLMASALFQGSIGPLIDLAFIDPGLIIGAFVATSLAFACFSAVAL
HVBI-1	(87)	RFGLLMGAALLEGASVGPLIELAIDFDPSILVTGFVGTIAIAFGCFSGAAI
NtBI-1	(91)	RIALLMAAALFKGASIGPLIELAIDFDPSIVIGAFVGCFAVFCFSAAM
OsBI-1	(90)	RFGILLAAALLEGASVGPLIKLAVDFDSSILVTAFVGTIAIAFGCFTCAAI
TaBI11	(1)	-----AAI
TaBI18	(83)	RFGLLMGAALLEGASVGPLIELAIDFDPSILVTGFVGTIAIAFGCFSGAAI
TaBI5 new	(57)	EVWAADGCSLLEGASVGPLIELAIDFDPSILVTGFVGTIAIAFGCFSGAAI
ZmBI14	(17)	RYWLLMAAALLEGASVGPLIKLAVEFDPSILVTAFVGTIAIAFACFSCAAM
ZmBI16	(30)	RYGLLMAAALLEGASVGPLVKLAVEFDPSILVTAFVGTIAIAFACFSGAAM
ZmBI33	(30)	RYGLLMAAALLEGASVGPLVKLAVEFDPSILVTAFVGTIAIAFACFSGAPW
ZmBI8	(1)	-----VIDLDSRILVTAFVGTAVAFACFSGAAI
Consensus	(101)	R LLMAAALLEGASVGPLI LAIDFDPSILVTAFVGTIAIAFACFSGAAI

Fig. 1a

	151	200
AtBI-1	(139)	LARRREYLYLGGLLSSGLSMLMWLQFASSIFG-GSASIFKFELYFGLLIF
BnBI-1	(139)	LARRREYLYLGGLLSSGLSMLMWLQFASSIFG-GSASIFKFELYFGLLIF
GmBI2	(140)	VARRREYLYLGGLVSSGLSILLWLHFASSIFG-GSTALFKFELYFGLLVF
GmBI3	(151)	VARRREYLYLGGLLSSWLSILMWLHSDSSLFG-GSIALFKFELYFGLLVF
HVBI-1	(137)	IAKRREYLYLGGLLSSGLSILLWLQFVTSIFGHSS-GSFMFEVYFGLLIF
NtBI-1	(141)	VARRREYLYLGGLLSSGLSILFWLHFASSIFG-GSMALFKFELYFGLLVF
OsBI-1	(140)	VAKRREYLYLGGLLSSGLSILLWLQFAASIFGHST-GSFMFEVYFGLLIF
TaBI11	(4)	IAKRREYLYLGGLLSSGLSILLWLQFATSIFGHSS-GSFMFEVYFGLLIF
TaBI18	(133)	IAKRREYLYLGGLLSSG-----LTIL
TaBI5 new	(107)	IAKRREYLYLGGLLSSGLSILLWLQFATSIFGHSS-GSFMFEVYFGLLIF
ZmBI14	(67)	VAKRREYLYLGGLLSSGLSILLWLQFAASIFGHQSTSSFMFEVYFGLLIF
ZmBI16	(80)	VARRREYLYLGGLLSSGLSILLWLQLAASIF-GHSATSFMEVYFGLLIF
ZmBI33	(80)	WQAR-EYLYLGCSRSGSPSCSGCSSPPSS--ALRNSFMFEVYFGLLIL
ZmBI8	(29)	IAKRREYLYLGGLLSSGLSILLWLQFATSIFGHTS-ATFMFEVYFGLLVF
Consensus	(151)	VAKRREYLYLGGLLSSGLSILLWLQFASSIFG S ASFMFEVYFGLLIF
	201	250
AtBI-1	(188)	VGYMVVDVTQEIIIEKAHLGDMDYVKHSLTLFTDFVAVFVRILIIMLKNSAD
BnBI-1	(188)	VGYMVVDVTQDIIIEKAHLGDMDYVKHSLTLFTDFVAVFVRVLIIMLKNSAD
GmBI2	(189)	VGYIVVDVTQEIVERAHLGDLVDYVKHALTLFTDLVAVFVRILVIMLKNSTE
GmBI3	(200)	VGYVIVDTQEIIERAHFGDLVDYVKHALTLFTDLAAIFVRILIIMLKNSSE
HVBI-1	(186)	LGYMVYDTQEIIERAHHGDMDYIKHALTLFTDFVAVLVRVLIIMLKNSAGD
NtBI-1	(190)	VGYIIFDTQDIIIEKAHLGDLVDYVKHALTLFTDFVAVFVRILIIMLKNASD
OsBI-1	(189)	LGYMVYDTQEIIERAHHGDMDYIKHALTLFTDFVAVLVRILVIMLKNSAD
TaBI11	(53)	LGYMVYDTQEIIERAHHGDMDYIKHALTLFTDFVAVLVRILIIIMLKNSAGD
TaBI18	(154)	L-----
TaBI5 new	(156)	LGYMVYDTQEIIERAHHGDMDYIKHALTLFTDFVAVLVRVLIILLKNAAD
ZmBI14	(117)	LGYMVYDTQEIVIERAHHG-----
ZmBI16	(129)	LGYVVYDT-----
ZmBI33	(127)	LG-----
ZmBI8	(78)	LGYMVYDTQEIIERAHRGDMDYIKHALTLFTDFVAVLVRILVIMMKNAQE
Consensus	(201)	LGYMVYDTQEIIERAH GDMDYIKHALTLFTDFVAV VRILIIIMLKNA D
	251	300
AtBI-1	(238)	KEEKKKKRRN-----GDVK-I-LYGCYRVWPL-RYYLLALSIGDQTCF
BnBI-1	(238)	KEDKKKKRRN-----D-KVRKKAK-SGCYVCFKK-----KRVG
GmBI2	(239)	RNEKKKKRRD-----
GmBI3	(250)	RNEKKKKRRD--ADRPTRAQASLQ-FSLWRIHN-----LFR-CWSLV-
HVBI-1	(236)	KSEDKKKKRKG-----S-----
NtBI-1	(240)	KEEKKKKRRN----CISGYSKTL-L-NLAFSCS---TSVDLRQVCC--FG
OsBI-1	(239)	KSEEKKKKKRS-ELLFPLCT-EKTTAAIASTYYDRAALQLGFMVNTSSFA
TaBI11	(103)	KSEDKKKKKRRS-----
TaBI18	(155)	-----
TaBI5 new	(206)	KVGGQEEEEEEKS-----
ZmBI14	(135)	-----
ZmBI16	(137)	-----
ZmBI33	(129)	-----
ZmBI8	(128)	KSQDEKKRK-----
Consensus	(251)	K E KKKRR

Fig. 1b

```

                                301                                350
AtBI-1 (278) H-KG-SACFTSAQVPSSDCK-----LECCSSFHKLFFKSL
BnBI-1 (269) VISTDMIALVFFTCLEQFW-----QHTLRICVFLLVTPDCEWI
GmBI2 (249) -----
GmBI3 (288) LVS YVFAVMVNVRI SFKHLHMYLPIS-CVV-HHTLV-KKKKKKKKKKKKK
HVBI-1 (248) -----
NtBI-1 (279) NASD-AARLCYAA CQCGYGGT-MVLF----PKHTIK-HACLHYIDNLRVY
OsBI-1 (287) FC-YGVNLLRFVVVVALQILACYMTRIFL-WWSR-SKRENTSSFATNLFA
Consensus (301)

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```

                                351                                400
AtBI-1 (312) VLLIASYQAKNNVGK-----SCLNFLKCVHFRKKKKKKKKK-----
BnBI-1 (307) SILKLC-KLSVGS-----
GmBI2 (249) -----
GmBI3 (335) KKKKKXXXXXXXXXXXXX--XXXXXGVCGLRYSRHSSNH-EGSLW-PGLC-
HVBI-1 (248) -----
NtBI-1 (322) YLFLLPFAVLGCS-LYS-FSVMLDHLLS-RLISHIDGRNENSHRRPNL FK
OsBI-1 (334) FW-LMMILSPKKKK-----
Consensus (351)

```

```

                                401                                450
AtBI-1 (348) -----
BnBI-1 (319) -----
GmBI2 (249) -----
GmBI3 (380) ACIDTVH-FGCNLCANS-YNVE-FI-EK-EEEEERLIG-PIAMCRVIW FV
HVBI-1 (248) -----
NtBI-1 (369) TEAQL-----
Consensus (401)

```

```

                                451                                500
GmBI3 (424) ENT-LAV-KLLVPLCS--LAMCLL-W-MSGFLLNIFICIC--S-YIV-TS
Consensus (451)

```

```

                                501                                512
GmBI3 (464) FLGLKKEKKKKK
Consensus (501)

```

Fig.1c

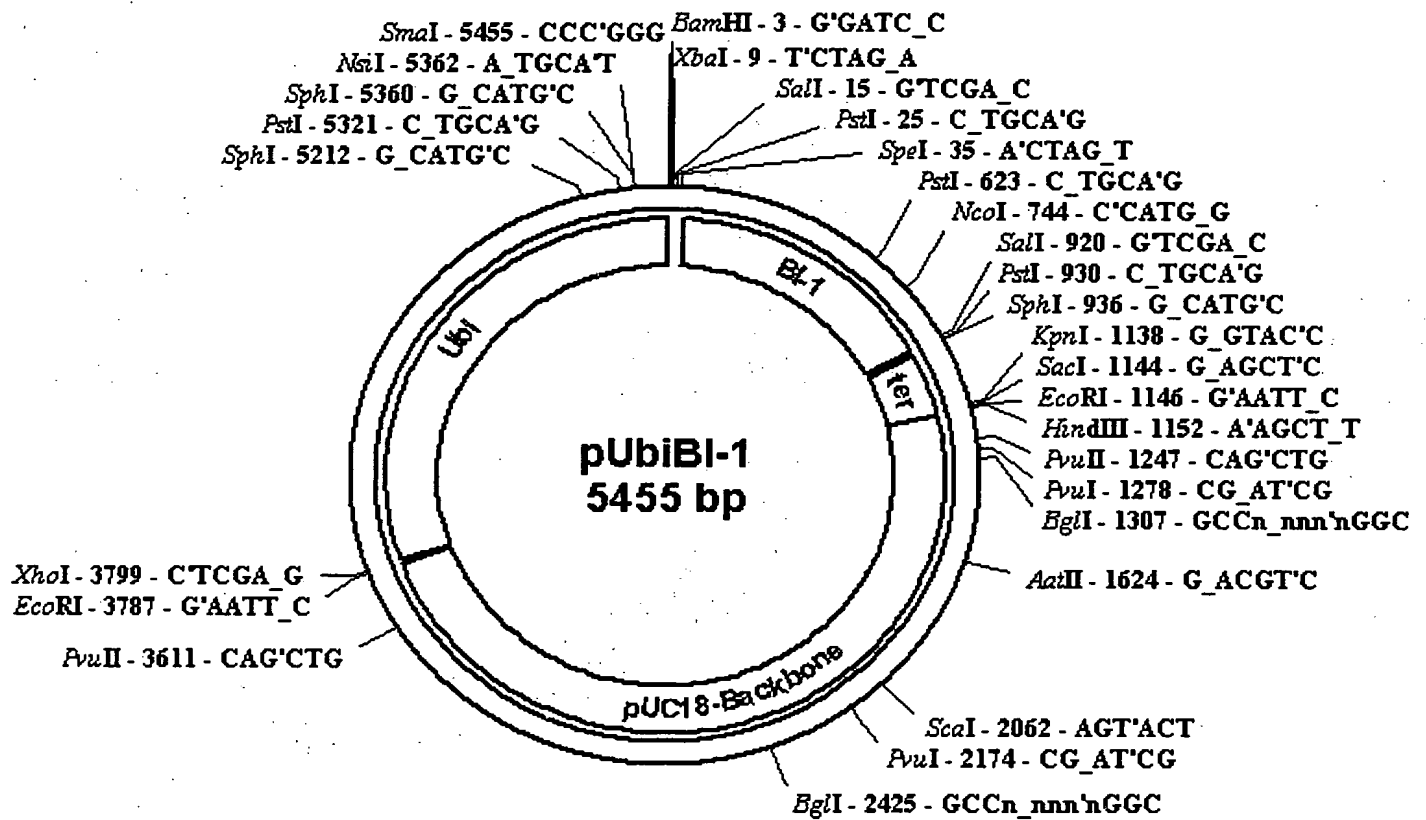


Fig. 2

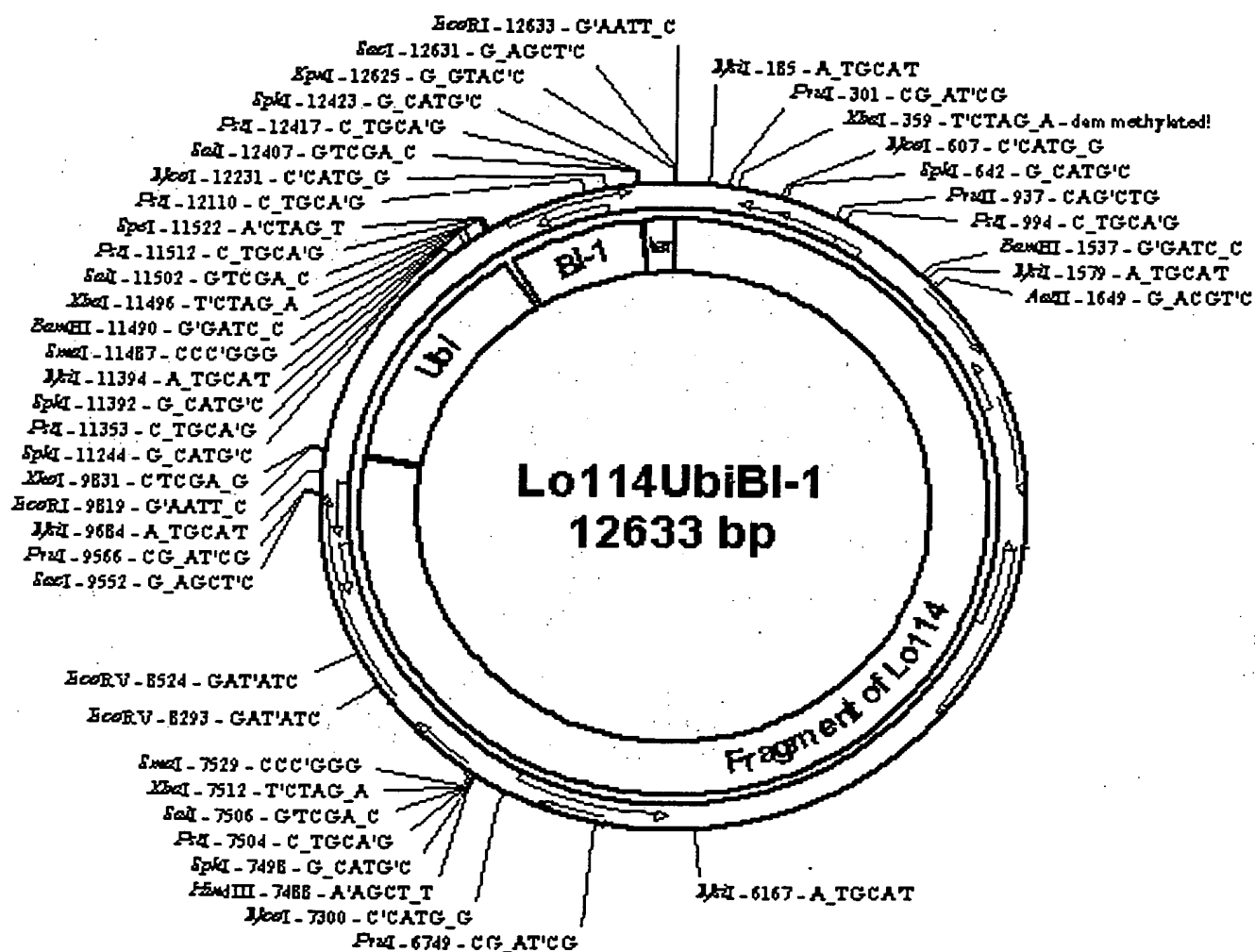


Fig. 3

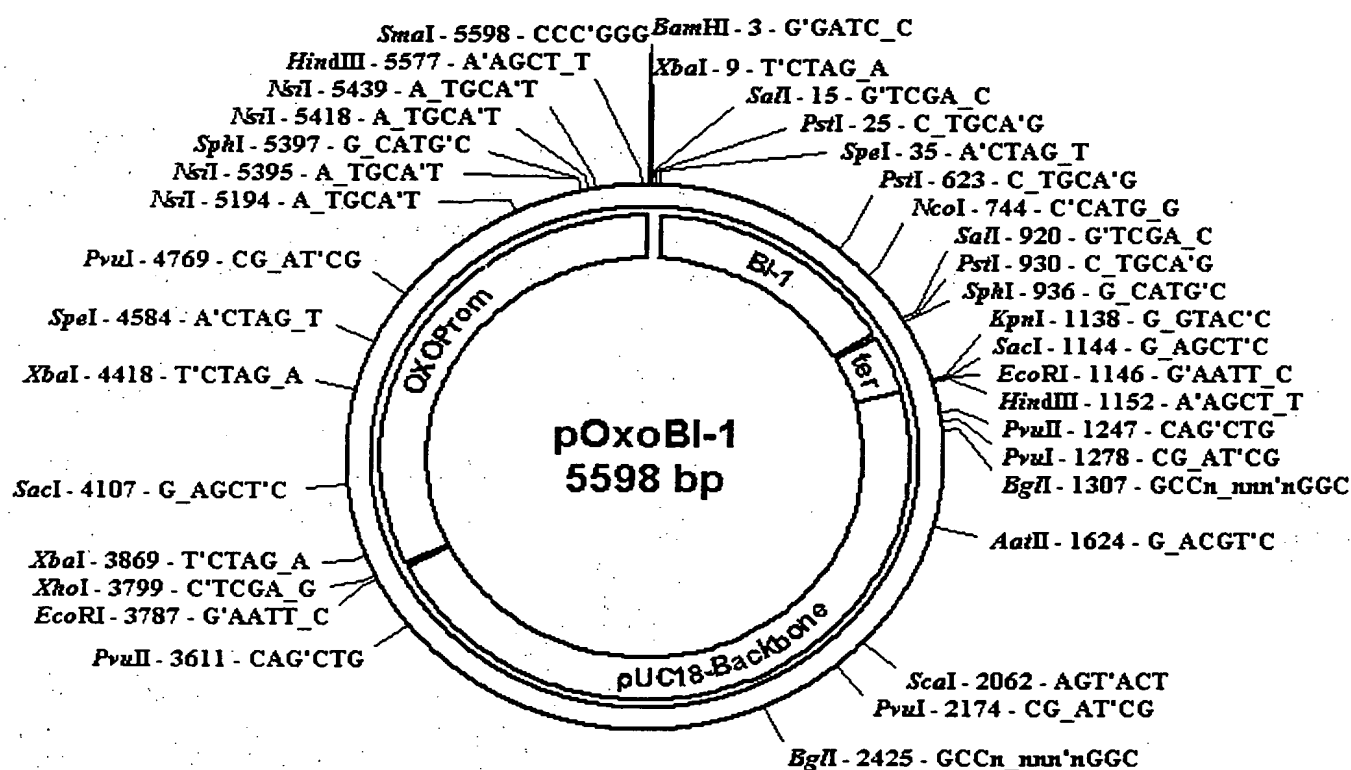


Fig. 4

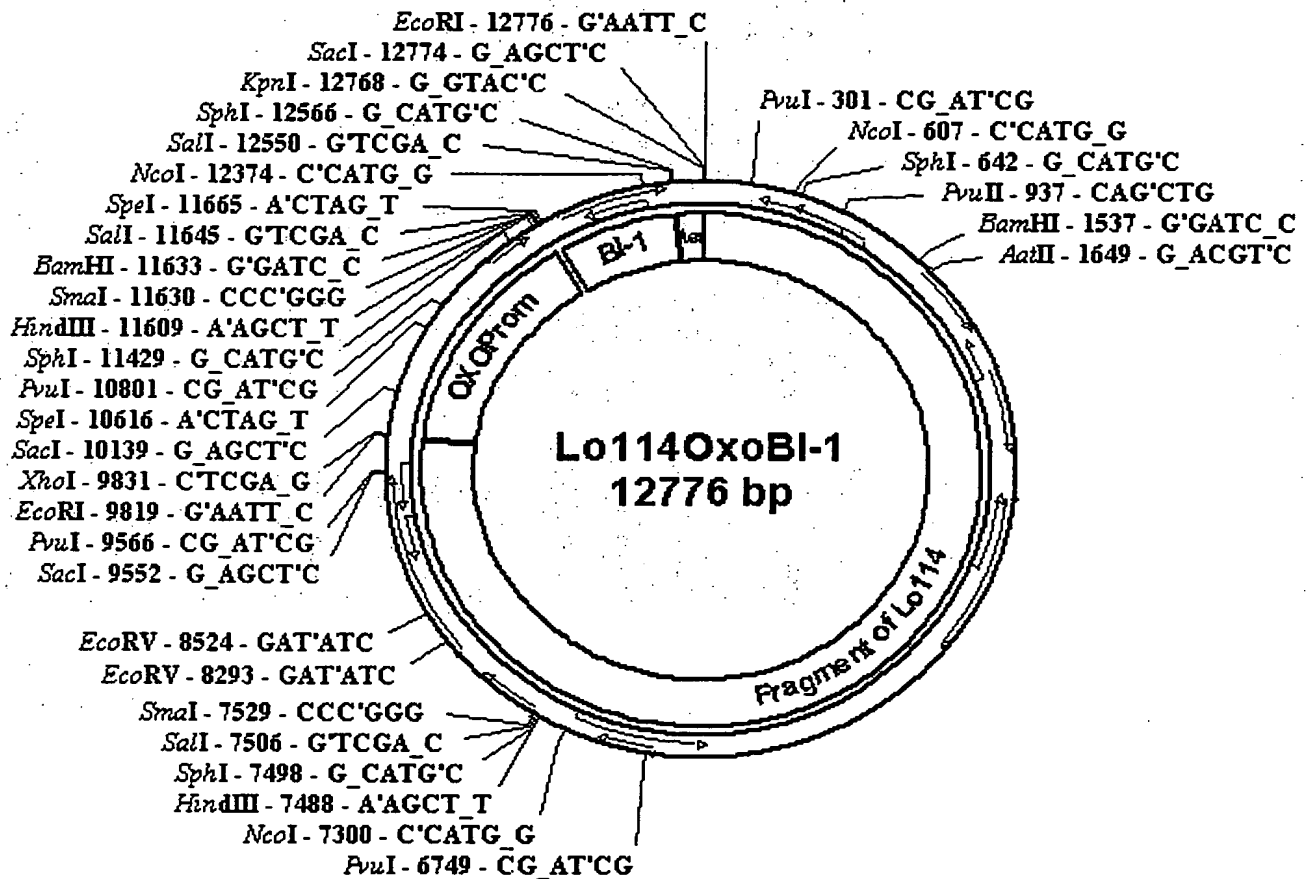


Fig. 5

H. vul. MDAFYSTSS---AAASGWHGDSLKNNFRQISPAVCSHLKLVYLTLCFALASSAVGAYLHIA 57
O. sat. MDAFYSTSSAYGAAASGUGYDSLKNNFRQISPAVCSHLKLVYLTLCVALAASAVGAYLHVA 60
A. tha. MDAFSSFFDS-OPGSRSSYSLSLKNNFRQISPAVQNHVKRVYLTLCALVASAFGAYLHVL 59
H. sap. MNIFDRKIN-----FLALLKESHITPSTQCHLKKVYASFALCMFVAAGAYVHMV 50

H. vul. LN--IGGMLTMLACVGTIAMMFVSPVYEE--RKRFGLLMGAAALLEGASVGPLIELAIDFD 113
O. sat. LN--IGGMLTMLGCVGSIAMLFSVPVFEE--RKRFGILLAAALLEGASVGPLIKLAVDFD 116
A. tha. WN--IGGILTTIGCIGTHIWLSCPPYEH--QKRLSLLFVSANLEGASVGPLIKVAIDVD 115
H. sap. THFIQAGLLSALGSLILMIWLMATPHSHETECKRLGLLAGFAFLTCVGLGPALEFCIAVN 110



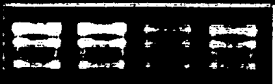



H. vul. PSILVTGFGVGTAFAGCFSGAIIIAKRREYLYLGCLSSGLSILLWLOFVTSIFGHSSGS 173
O. sat. SSILVTAFVGTAFAGCFTCMAIVAKRREYLYLGCLSSGLSILLWLOFAASIFGHSTGS 176
A. tha. PSILITAFVGTAFVCFSAAMLAERREYLYLGCLSSGLSMIMWLOFASSIFGGSASI 175
H. sap. PSILPTAFMGTAIETCFETLSALYARRESYLFLGGILMSALSLLLSSLGNVFFG-SIWP 169

H. vul. FMFEVYFGLLIIFLCYHVYDTQEIIEKAHHGDMDYIKHALTLFTDFVAVLVRVLIIMLKNA 233
O. sat. FMFEVYFGLLIIFLCYHVYDTQEIIEKAHHGDMDYIKHALTLFTDFVAVLVRILVIMLKNA 236
A. tha. FKFELYFGLLIIFVGYHVYDTQEIIEKAHLGDMDYVKEHSLTLFTDFVAVFVRILIMLKMS 235
H. sap. EQANLYVGLVVMCGFVLVDTCLEIEKAHEHGDQDYIWHCIDLFLDFITDFRKLHMLAMME 229

H. vul. GDRSEDKKRKRGS 247
O. sat. SDRSEEKKRKKRS- 249
A. tha. ADR-EEKRKKRRN- 247
H. sap. KDR---KREKK--- 237

Fig. 6

rRNAs

	\emptyset	Pallas
	inoculated	
	\emptyset	BCP <i>Mla12</i>
	inoculated	
	\emptyset	BCP <i>mlo5</i>
	inoculated	
<div>0 1 4 7</div> <hr/> <div>dai</div>		

BI-1







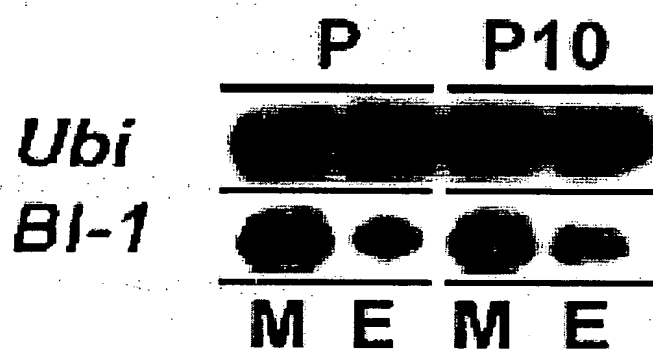
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	\emptyset	BCP <i>Mla12</i>
	inoculated	
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	inoculated	
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Fig.7

**Fig. 8**

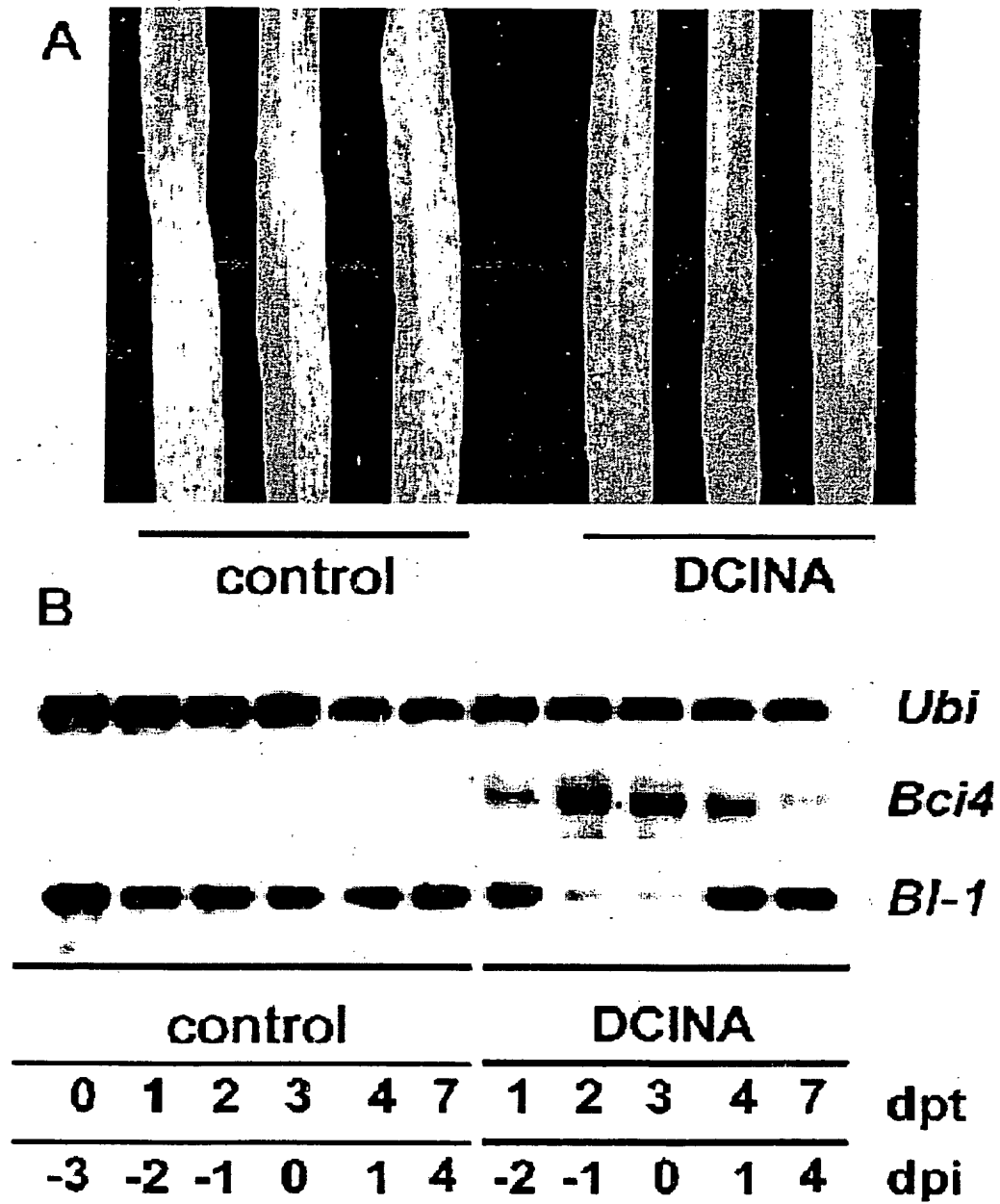
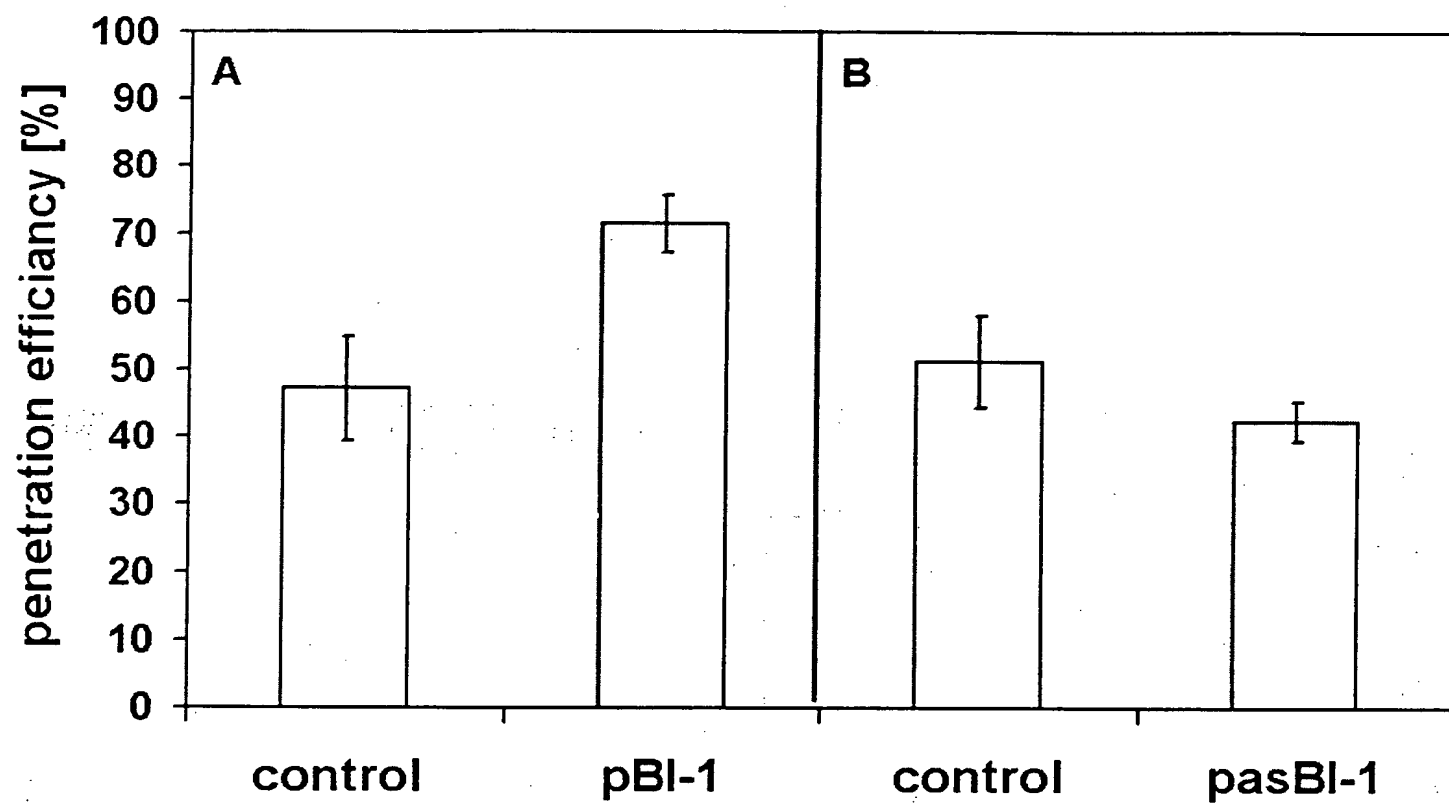
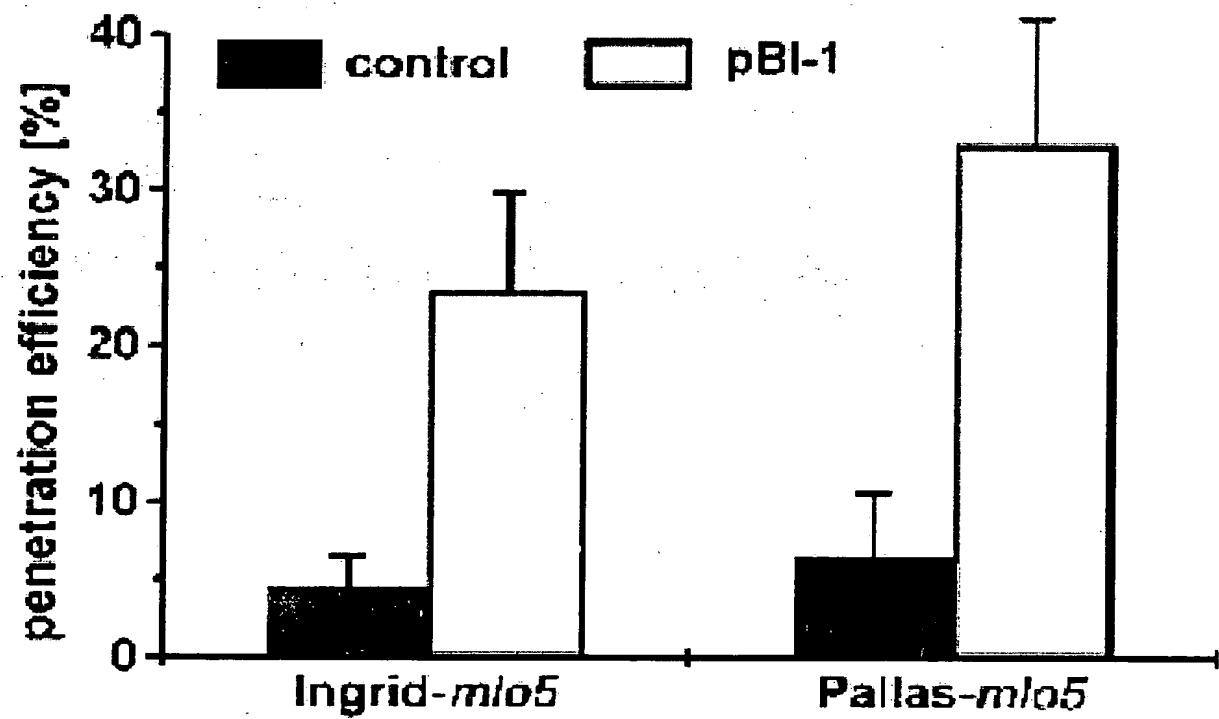


Fig. 9

**Fig.10**

**Fig.11**

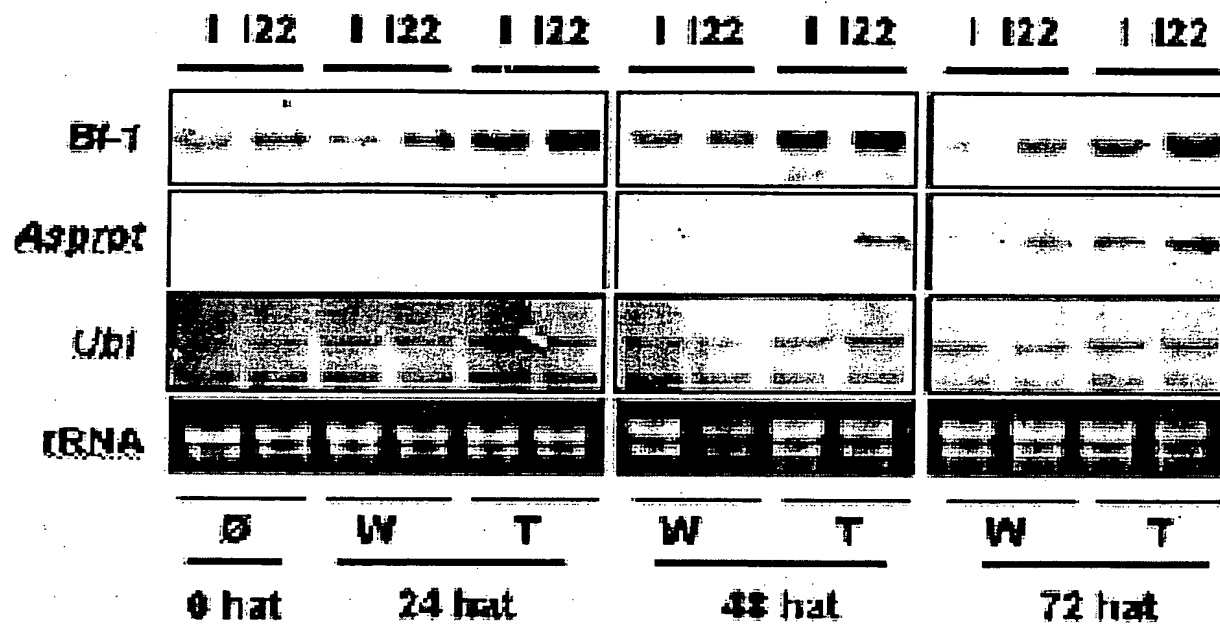


Fig.12

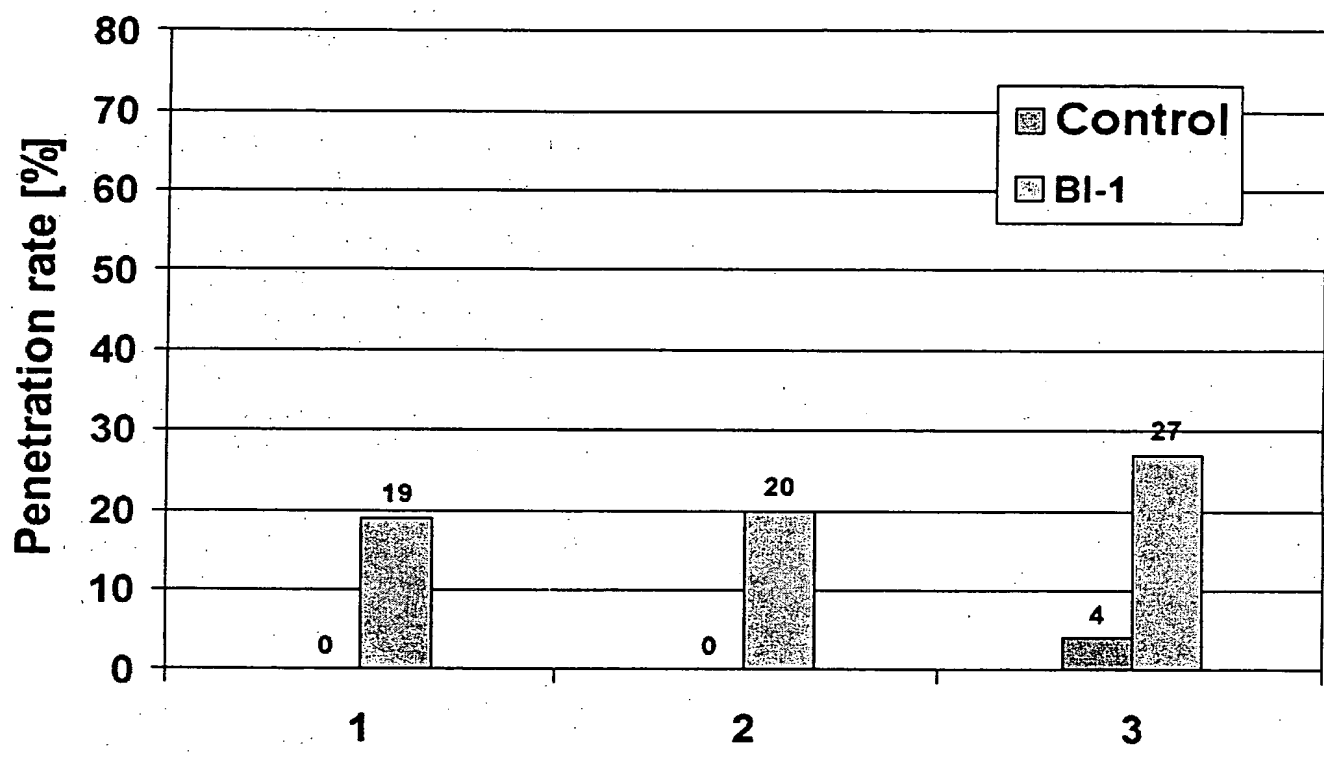


Fig.13